National Program 301 • Plant Genetic Resources, Genomics, and Genetic Improvement
FY 2012 Annual Report

The USDA-Agricultural Research Service's (ARS) National Program (NP) 301, Plant Genetic Resources, Genomics, and Genetic Improvement, supports research that maintains, protects, enhances, and expands the United States genetic resource and information base, and increases knowledge of the structure and function of plant genes, genomes, and biological and molecular processes. Through innovative research tools and approaches, this National Program manages, integrates, and delivers vast amounts of genetic, molecular, biological, and phenotypic information to a diverse global clientele. The ultimate goals for the preceding efforts are to improve the production efficiency, yield, sustainability, resilience, health, product quality, and value of U.S. crops. This National Program addresses the need to:

- Ensure the long-term safety and integrity of our agriculturally valuable genetic resource collections and associated information;
- Develop novel approaches for analyzing complex traits, identifying favorable genes underlying those traits, and deploying them in breeding stocks;
- Exploit new technologies that enhance traditional methods of genetic improvement;
- Genetically improve a broad spectrum of major, specialty, and new crops;
- Increase our knowledge of the structure and function of crop genomes and of plant biological and molecular processes; and
- Acquire, analyze, and deliver genetic and information resources to research communities and to the public.

Genetic resources are the foundation of humanity's agricultural future. ARS genebanks contain sources of resistance, tolerance, and adaptation to biotic and abiotic stresses and new genes to improve the quantity, quality, and production efficiency of our food, feed, bioenergy, fiber, and ornamental crops. To ensure those genes are available for research and breeding, ARS must continue to strategically acquire and conserve germplasm that contains them; develop new screening methods for identifying favorable traits; ensure that germplasm is distributed where and when it is needed; and safeguard these collections for future generations.

ARS has taken a leadership role in developing and curating crop genomic and phenotypic databases, which are expanding now and will continue to do so in the future. New tools are needed to efficiently capture phenotypic data and extract useful information, via innovative data-mining strategies, from the ever-increasing flow of data into these databases. Methods to interconnect databases containing diverse types of information are needed to more efficiently and effectively identify important properties of genes and genomes and apply that knowledge to crop improvement. In addition, these interconnected databases will enable researchers to better associate specific genes with agriculturally-important traits and build on genetic advances in one crop to speed genetic gain in others.

For major, specialty, and new crops, ARS, in close cooperation with diverse public and private sector collaborators, will improve and broaden the genetic base of U.S. crops to reduce genetic vulnerability. NP 301 scientists will devise and apply new technologies to develop superior new crop varieties and enhanced germplasm and will accelerate the deployment of high-value traits into breeding populations. New genetic sources of key crop traits will be identified and incorporated into crop breeding lines and gene pools. New breeding theories and strategies that exploit the vast amount of available genotypic data will be developed to effectively capture the intrinsic genetic potential in germplasm. To do so, innovative tools will be developed for dissecting the

architecture of complex crop traits. These tools will be applied to mapping and determining the function of underlying genes so that variation in them, and in linked genomic sequences, can be exploited as more precise genetic markers. This knowledge will also enable molecular and genetic variability to be associated with specific phenotypes to enhance the effectiveness of genomic selection, thereby accelerating and strengthening progress in crop genetic improvement.

Plant breeding has a long history of improving crops through phenotypic or marker-assisted selection, usually in the absence of information regarding underlying genes or gene networks that control key traits, or that control how plants interact with their environment. Understanding the key biochemical pathways and the underlying controls for plant growth, development, and metabolism has been elusive. However, recent advances in plant molecular biology, genetic engineering, and physiology could create opportunities for improvement of crops by more precisely and rapidly manipulating the existing variability in plant properties, or by creating new variability when warranted. Knowledge of how to precisely modify biological mechanisms will contribute not only to advances in fundamental plant biology, but will also help identify potential unintended consequences of that manipulation.

In addition to conducting research, ARS and its university cooperators will continue to mentor and train the next generation of crop breeders, geneticists, bioinformaticists, genome researchers, and genetic and genomic resource and information managers. Developing the next cohort of researchers is particularly important, considering the projected strong demands for these scientific personnel.

This National Program is composed of three Research Components (see below) and their constituent Problem Statements. Notably, these categories do not act as barriers or "stovepipes" that impede research across the National Program. Rather, many of the individual research projects and resources contribute to the goals of several NP 301 Research Components, or even several National Programs:

- Crop Genetic Improvement (plant breeding, genetic enhancement, molecular marker and trait analyses, nucleotide sequencing, and genetic mapping).
- Crop Genetic and Genomic Resources and Information Management (conserving a broad spectrum of genetic resources and facilitating their use; maintaining and delivering genetic resource, genomic, and genetic data via databases and information management systems; and devising new analytical tools that compile, dissect, interrelate, manage, and visualize the large datasets).
- Crop Biological and Molecular Processes (fundamental – often high-risk – research to generate an enhanced knowledge base and devise superior research tools that ultimately contribute to greater crop productivity and efficiency; better product quality and safety; improved protection against pests and diseases; enhanced tolerance to abiotic stress; and sustainable practices that maintain or enhance environmental quality).

Component 1 – Crop Genetic Improvement

Tomato genomes sequenced. The full genome sequence for a crop constitutes a powerful research tool, most importantly by enabling breeders to accelerate the development of superior varieties. Tomato, one of the most important vegetables globally, provides key vitamins and minerals to populations worldwide and generates billions of dollars of economic value in the United States. The International Tomato Genomics Consortium led by ARS scientists from Ithaca and Cold Spring Harbor, New York, sequenced the genomes of the domesticated tomato and its wild ancestor, generating an invaluable knowledgebase for uncovering the genetic bases for tomato fruit taste, quality, size, yield, nutritional content, and host-plant resistance to diseases, pests, and environmental extremes. Access to this new knowledge should enable tomato breeders

and geneticists to enhance the efficiency and effectiveness of tomato breeding for key, high-value horticultural traits.

More than 150 corn traits mapped to specific regions of the corn genome. ARS corn researchers in Columbia, Missouri; Ithaca, New York; and Raleigh, North Carolina, completed extensive evaluations of biochemical and agronomic traits for 5,000 corn lines that collectively included much of the total variation found in the corn breeding gene pool. These evaluations located the regions of the corn genome associated with more than 150 traits of major agronomic importance. Also, ARS researchers in Ithaca, New York, characterized more than 55 million variable regions in the corn genome as a first step for identifying genetic markers for breeding those traits, or the actual genes controlling the traits. All this important new information and corn genetic stocks are accessible through the Maize Genome Database. The data, and analytical ("informatics") tools for managing those data and relating them to other genome data for other plants, will enable geneticists and breeders to more rapidly identify genes for improved crop performance, quality, and yield.

New wheat germplasm developed with more effective resistance genes to Ug99 stem rust from wild wheat relatives. Stem rust strain Ug99 threatens wheat production worldwide. ARS researchers in Manhattan, Kansas, and in St. Paul, Minnesota, along with Kansas State University collaborators, developed a wheat germplasm line with Ug99 resistance gene (Sr47) derived from a wild wheatgrass species. ARS researchers in Fargo, North Dakota, and in St. Paul, Minnesota, used chromosome engineering techniques to successfully transfer small segments of goatgrass chromosomes carrying the Ug99-resistance gene (Sr47) to durum wheat. The sources of the wild wheat relatives were seeds safeguarded in the USDA Small Grains Repository in Aberdeen, Idaho. These new lines with highly effective resistance genes from the wild relatives of wheat will help wheat breeders throughout the world develop more durable protection of the global grain supply.

Rice grain yield increased 25 percent by genes from wild species. Most cultivated rice belongs to the species *Oryza sativa*. However, breeders have crossed that species with wild relatives of rice to enhance pest and disease resistance. ARS scientists in Stuttgart, Arkansas, and Cornell University researchers determined if these wild species are genetic reservoirs for new grain yield enhancing genes. When genes from the wild rice species *Oryza rufipogon* were crossed into the commercial rice cultivar Jefferson, two genetic insertions from *Oryza rufipogon* in the Jefferson genome increased grain yield by 25 percent. These results demonstrated that wild ancestral species, with no obvious agronomic merit, are an important genetic resource for improving the yield potential of cultivated rice.

Completion of a draft citrus genome. The sequencing of the complete genome of crop plants provides a foundational scientific tool for characterizing crop gene structure and evolution as well as for identifying genes for crop improvement. ARS scientists in Albany, California, completed a draft genome of the citrus rootstock Carrizo with sufficient coverage (15X) to enable assembly of approximately 80 percent of the genome. The Carrizo genome contains the only known source of resistance to citrus greening disease in citrus, a disease that has the potential to eliminate the juice processing industry in Florida. Potential citrus greening-resistance genes have been identified in the Carrizo genome and are being prepared for testing in cooperation with ARS scientists in Fort Pierce, Florida.

Identifying a sorghum gene for superior livestock feed and bioenergy value. Lignin is the principal substance that makes cell walls resistant to breakdown either by livestock digestive systems or during the cellulosic bioenergy conversion process. The mutant gene brown midrib 2 (*bmr2*) reduces lignin content and alters the lignin composition of sorghum cell walls. The specific genetic mutation causing *bmr2* was identified by ARS researchers in Lincoln, Nebraska, and their colleagues at the University of Florida as affecting an enzyme involved in lignin synthesis. The function of the enzyme was characterized and determined to be largely responsible for an initial step in lignin synthesis. This new information about the *bmr2* gene can be applied to

manipulate lignin content in sorghum and to improve that crop as a source of animal forage and as a bioenergy feedstock.

Construction of a new high-quality cotton genetic map. ARS researchers in New Orleans, Louisiana, and U.S. and French colleagues constructed a new, high-quality (termed an ultra-dense or "UD") genetic map for commercial "Upland" cotton by combining six separate "high density" maps, including more than 8,200 unique DNA markers. Statistical comparisons of those mapped markers with the smaller and simpler genome sequence of a wild cotton species revealed strong structural similarities so that information from the simpler genome can be applied to locate genes or other genetic features on the larger genome of "Upland" cotton. This UD map is a valuable resource for mapping the genes controlling complicated traits such as fiber yield and quality, isolating and "cloning" key cotton genes, and understanding more comprehensively cotton genome structure and evolution. It will also serve as the standard reference and starting point for additional research on the structure of the genomes of different cotton populations and species.

Release of a high yielding and high beta-glucan food barley. Barley which is bred specifically as a source of nutritious human food products has a great potential to benefit farmers, the food industry, and consumers. ARS researchers in Aberdeen, Idaho, developed and released 'Transit' barley, a specialty food-grade variety that combines very high levels of heart-healthy beta-glucan with good productivity characteristics. 'Transit' has attracted significant interest from producers and the food industry, demonstrating the value of a concentrated source of beta-glucan fiber. 'Transit' is expected to create new opportunities for farmers and the food industry to efficiently bring healthy products to market.

New genetic stock with Fusarium Head Blight (scab) resistance developed for durum wheat. Fusarium Head Blight (FHB), often called scab, is a damaging disease of durum wheat for which there is no reliable source of resistance for current durum cultivars. ARS researchers in Fargo, North Dakota, used a wild grass species as a source of FHB resistance to produce plants in which one pair of durum chromosomes was replaced by a pair of wild grass chromosomes. This unique genetic stock will accelerate breeding durum wheat with FHB protection.

Development of soft white winter and soft white club wheats with protection to stripe rust losses. Evolving stripe rust strains threaten wheat yields in the Pacific Northwest. ARS wheat researchers in Pullman, Washington, applied marker-assisted selection to develop new wheat varieties with excellent resistance to stripe rust, combined with soil borne disease resistance and excellent agronomic and end use quality characteristics. These new varieties will reduce grower risk and benefit growers and end users by saving money on fungicide sprays and providing wheat grain that is highly marketable.

Construction of a saturated genetic map for marker identification in peanut. A saturated genetic linkage map can help peanut breeders to visualize the structure of peanut genomes and accelerate peanut cultivar selection. ARS scientists in Tifton, Georgia, developed this saturated map, incorporating 249 loci distributed on 23 linkage groups. This map was applied to pinpoint the location of a genetic locus linked to tomato spotted wilt virus resistance, as well as three major genetic loci linked to late leaf spot resistance. It also confirmed the relative contribution of two known genes implicated in controlling the high oleic trait in peanuts, and will likely continue to make selection more precise in peanut breeding.

Release of grape varieties and rootstock. Seedless table grape cultivars with superior productivity and storage quality are needed for commercial production in California. Nematodes, a major pest for grape production, reduce yields and plant vigor making vineyards uneconomical. ARS has released two table grape varieties and one rootstock following extensive development and testing in Parlier, California: Valley Pearl, a white seedless table grape for the early to mid-season that is high yielding with superior good storage quality; C51-63, a very productive, late ripening red seedless grape with desirable berry size and storage ability; and

Demko 10-17A, a grape rootstock with a moderately vigorous rootstock that protects against many nematodes as well as phylloxera. These releases will contribute to the continued productivity of U.S. table grape growers and the availability of high quality grapes for consumers.

The first recombinant inbred line (RIL) population in beet. Precise genetic analyses of agronomic and other traits of sugar and table beets are very difficult because these plants are open-pollinated by the wind. ARS researchers in East Lansing, Michigan, began 12 years ago to inbreed populations of beets to assist with general genetic analyses, mapping of single gene traits, and dissection of traits important for the production, profitability, and expansion of beet products to new markets. These populations were analyzed to determine the genetics of morphological characters that define differences between sugar beet and red table beet as well as define the minimum number of genes that contribute to economic sucrose production of sugar beet. These "recombinant inbred line" populations of beet demonstrate that deeply inbred sugar beet germplasm can be created for precise and repeatable molecular determinations of agronomic traits that will lead to improved varieties.

Genetics of salad-cut lettuce shelf-life. Lettuce with commercially acceptable or extended shelf-life must be bred to sustain the market for packaged salads, which is vital to lettuce producers and this industry. ARS researchers in Salinas, California, determined the genetics of leaf decay, which in an experimental population is inherited as a major quantitative trait locus (QTL) describing 30 to 80 percent of the differences (depending on the experiment) in decay. Breeding for reduced decay in lettuce is now feasible because the trait is conditioned by few QTL with minimal environmental effects.

New pinto bean line with partial resistance to white mold disease. White mold, the number one disease problem of dry bean in the United States, is especially damaging to pinto bean, the most important market class. ARS researchers in Prosser, Washington, and collaborators at Michigan State University and University of Nebraska, developed and released "USPT-WM-12" pinto bean germplasm line with partial resistance to white mold disease. This line has performed exceptionally well under severe white mold pressure in national trials in 2010 and 2011, with better yield performance and better overall resistance to white mold than earlier germplasm. This new line enables breeders to develop pinto bean cultivars with improved resistance to white mold which will save growers millions of dollars from lost production.

Release of Potato Variety Teton Russet – an early maturing variety suitable for processing and fresh consumption. The U.S. potato industry needs improved varieties for Russet Norkotah, the second-most widely grown potato variety in the United States. Teton Russet, an early maturing potato variety originated from the ARS potato breeding program in Aberdeen, Idaho, was developed and released with collaborators in the Tri-State Potato Variety Development Program. Teton Russet has resistance to two important diseases, common scab and dry rot; high protein and Vitamin C content; and a low concentration of the amino acid asparagine which contributes to lower acrylamide concentrations in its processed potato products. It thus provides a superior alternative to the variety Russet Norkotah.

New sugarbeet germplasm with improved processing properties. Sodium, potassium, and amino-nitrogen accumulate in sugar beet roots and impede sucrose recovery during normal processing. ARS researchers in Fargo, North Dakota, released three germplasm lines with substantially reduced levels of each of these substances. These lines, the result of numerous plant breeding cycles conducted in conjunction with chemical analysis of individual roots, will provide germplasm for future improvement in sugar beet processing quality and sucrose recovery, thereby increasing grower profits and improving factory efficiency.

Release of new sugarcane variety with disease/pest resistance and high yields. Varieties are the life-blood of the sugarcane industry in Louisiana, and a continuous pipeline of new varieties is needed to sustain that industry. Researchers at the Sugarcane Research Unit in Houma, Louisiana, selected, evaluated, and released

to the Louisiana sugarcane industry the variety Ho 05-961. The new variety produces sustained yields through the third harvest, particularly in sugar per acre. It is resistant to the diseases rust, smut, leaf scald, and both the sugarcane borer and Mexican rice borer. Therefore it is an appropriate variety for planting in areas not suited to insecticide application. The positive performance of Ho 05-961 for many important traits suggests that it will contribute to the economic sustainability of the sugarcane industry.

Watermelon Vine decline resistant germplasm line. Watermelon Vine decline, a serious disease that has plagued watermelon growers for the past several years, has resulted in losses of over $60 million in southwest and west central Florida. ARS scientists in Charleston, South Carolina, developed the watermelon germplasm line "392291-VDR" with resistance to this disease which is caused by a whitefly transmitted virus. This resistant germplasm line will enable breeders to develop watermelon varieties with resistance to this dreaded disease and help reduce insecticide use.

Development of improved tepary (Phaseolus acutifolius) germplasm. Improved lines of tepary, a desert species related to common bean with far higher levels of abiotic stress tolerance, have been developed by ARS scientists in Mayagüez, Puerto Rico, and colleagues from the University of Puerto Rico. These lines have larger seed size than most teparies and have multiple stress tolerance, including tolerance to high ambient temperature and drought, and resistance to bacterial blight. These lines could increase legume production in arid/high temperature environments directly and contribute to further tepary genetic improvement.

Component 2 – Crop Genetic and Genomic Resources and Information Management

New USDA Plant Hardiness Zone Map Released. The USDA Plant Hardiness Zone Map (PHZM) is an essential tool for the country's estimated 60 million gardeners, nurseries, horticultural producers, plant breeders, and government agencies that use it as a primary reference to define geographic patterns of extreme winter cold and identify plants that are most likely to thrive in a particular area. ARS researchers from Ames, Iowa, and colleagues from Oregon State University have completed a new 2012 edition of the PHZM which brought the map into the "Digital Age." It combined leading-edge geographical information systems analytical technology, internet/World Wide Web information delivery, and traditional horticultural and climatological scientific expertise and clientele input to transform what had been a static, paper map into a dynamic, Web-accessible, multi-functional interactive information resource. The PHZM Web site attracted more than 500,000 visitors during the first two weeks after release and more than 2 million visitors to date. The PHZM earned a Special Achievement in Geographical Information Systems (SAG) Award from Esri, Inc., one of 150 chosen for awards from 100,000+ Esri clients worldwide.

Identifying genes in tomato which originated from wild relatives. Tomato is unusual because of the many key horticultural traits that originated from its wild relatives. In addition to those traits, theory would predict that additional "hidden variation," genetically linked to such features, might also have been introduced into tomato breeding stocks. ARS researchers in Geneva, New York, applied new statistical genetic approaches to identify in tomato breeding stock such latent genes from wild relatives. They uncovered not only genes from wild relatives introduced into tomato through deliberate breeding, but also other genes simply genetically-linked to the target traits. Furthermore, previously unrecognized hybridizations in nature between tomato and wild relatives were identified. These results will enable even more detailed examinations of such genes introduced from wild relatives so that tomato genetic resources can be more effectively conserved and utilized in tomato breeding.

Seed longevity is detectable through non-invasive assays. ARS scientists in Fort Collins, Colorado, developed assays that noninvasively detect very early signs of seed deterioration during storage. Assays are based on volatile emission from seeds detected through gas chromatography of the storage headspace; seed oil

crystallization kinetics detected by differential scanning calorimetry; and molecular relaxations within seed structures detected from dynamic mechanical analysis. These sensitive non-destructive assays do not deplete samples of valuable germplasm that are normally consumed during viability monitoring tests. These assays help preserve seed supplies in long-term storage more efficiently and effectively than do traditional approaches.

Determining redundancy within the NPGS onion germplasm collection with genetic markers. Conserving genetically redundant accessions can constitute a suboptimal allocation of genebank curatorial resources and can reduce the efficiency of crop germplasm characterization, evaluation, and enhancement. ARS researchers in Pullman, Washington, and their collaborators found that patterns of genetic variability in two different types of genetic markers (simple sequence repeat (SSR) and targeted region amplified polymorphisms (TRAP)) led to sometimes different conclusions regarding the genetic identity and divergence among a set of 35 short-day onion accessions. These results underscored the importance of combining a sufficiently large genetic marker data set with passport information, and of patterns in morphological markers when examining genetic redundancy of problematic samples.

Documenting crop wild relatives occurring in the United States. More than 700 primary, secondary, and tertiary gene pool relatives for 20 of the most economically important crops were identified in the GRIN database. A Web interface (www.ars-grin.gov/~sbmljw/cgi-bin/taxcrop.pl) was constructed by ARS researchers in Beltsville, Maryland, to query and retrieve information about the occurrence of crop wild relatives in the United States to assist scientists in the United States and other countries with developing strategies for filling gaps in genebank collections, and for *in situ* conservation of crop wild relatives.

Genetic characterization of the NPGS cotton germplasm collection. ARS researchers in College Station, Texas, and Stoneville, Mississippi, and their collaborators genotyped more than 2,300 accessions, or approximately 25 percent of the total NPGS cotton collection, with 105 simple sequence repeat markers. They determined species introgression, redundancy among accessions, and within-accession variation with the markers. These data provide valuable information on the patterns and distribution of genetic diversity within the collection to guide curatorial decision-making and reveal sources of unique genetic variation to exploit for cotton improvement.

Genotyping assay developed for high oleic acid peanuts. ARS researchers in Griffin, Georgia, developed a real-time polymerase chain reaction genotyping assay for alleles of genes governing the high oleic acid trait in peanuts. This assay enables curators to identify particularly valuable accessions, and breeders to test seed or leaf tissue in initial crosses rather than via destructive chemical analyses of ground seeds. This rapid assay will help identify key genotypes linked to important agronomic traits, improve curatorial efficiency, and decrease the time and effort required to characterize the progeny of breeding crosses by eliminating undesirable seedlings.

Discovery of the third site in Mexico for a rare wild relative of maize. Some types of teosinte, the ancestor to maize, are generally cross-fertile with maize, enabling teosinte to serve as a potential source of genes for maize improvement. ARS scientists from Fort Collins, Colorado, and their collaborators in Mexico have found another field location for a rare wild perennial teosinte (*Zea perennis*) in Mexico. Previously, only two sites for this perennial species were known in Mexico. This find is significant as it represents a potentially unique population of this key evolutionary relative of maize.

Novel method for identifying different nitrogen-fixing bacteria and determining their benefits to soybean growth and production. Soybean benefits from symbiotic bacteria, referred to as "rhizobia," that occupy the roots and help the plant to produce its own nitrogen, thus eliminating the need for nitrogen fertilizer applications. The many different genetic types of rhizobia differ substantially in their ability to "fix" the

nitrogen required for soybean growth and production. Consequently, identifying the unique types of rhizobia in culture collections is a priority, as is determining how effectively the different types fix nitrogen in symbiosis with the soybean plant. ARS researchers in Beltsville, Maryland, developed novel methods for describing soybean rhizobia genotypes and analyzing how these bacteria occupy soybean roots so that genetic types of rhizobia in each root location can be identified, nitrogen fixing efficiency determined, and soybean varieties identified that form symbioses with the most efficient rhizobia.

Expansion of the switchgrass and other warm-season grass germplasm collections. The ARS warm-season grass collection for species native to the United States did not contain adequate genetic diversity to meet the needs of requesters. The switchgrass (*Panicum*) collection was expanded with 94 accessions collected by ARS researchers in Griffin, Georgia, from areas in the United States previously underrepresented. The newly collected switchgrass accessions were tested for germination, regenerated, characterized genotypically with SSR markers, and the ploidy levels were determined. These efforts provided well-characterized, readily available, and viable material to scientists for bioenergy feedstock development.

Component 3 – Crop Biological and Molecular Processes

Import of genetically-engineered (GE), PRSV-resistant 'Rainbow' papaya to Japan approved. A major portion of the U.S. market share of papayas sold in Japan was lost when the Hawaiian papaya industry was devastated in the 1990s by the papaya ringspot virus (PRSV). The first shipments to Japan of 'Rainbow,' a transgenic PRSV-resistant variety, occurred in December, 2011, following final regulatory approval by the Japanese government. The 'Rainbow' import application package was prepared and submitted through a collaborative effort involving ARS researchers in Hilo, Hawaii, and researchers or representatives from several U.S. universities and the papaya industry. 'Rainbow' papaya is the first fresh genetically-engineered fruit to be marketed commercially in Japan.

Identification of a novel mechanism regulating corn defense to insects. Damage caused by insect feeding causes yield losses and renders corn plants more susceptible to infection by fungal pathogens, including those which produce mycotoxins that can contaminate grain used for food or livestock feed. Knowledge of molecular mechanisms regulating defenses against insect feeding in crop plants is desirable, but little is known. ARS corn researchers in Gainesville, Florida, determined that a corn protein signal ZmPep3 conferred enhanced resistance to caterpillar damage. Results from studies using ZmPep3 indicate that this protein and related proteins in a number of other crop species can be used to activate plant anti-herbivore defenses and increase plant resistance to herbivore damage and subsequent pathogen infection.

Successful field trial of transgenic potatoes expressing a gene conferring resistance to multiple viruses. Potato viruses such as Potato Virus Y, Potato Virus X, Potato Virus A, and Potato Leaf Roll Virus seriously impact potato growers and processors in the United States by way of production losses and rejection of seed lots by seed certification agencies. ARS scientists in Albany, California, constructed an artificial gene designed to confer resistance to all four viruses and introduced it into Premier Russet, Norkotah Russet, and Atlantic potatoes. These potatoes were entered into a field trial in cooperation with ARS scientists in Aberdeen, Idaho, to determine virus susceptibility. The transgenic potatoes demonstrated field resistance to both Potato Virus Y and Potato Leaf Roll Virus indicating the success of this strategy for introducing multiple virus resistance.

Genes that control the production of a key component of grape varietal aroma are mapped. Meothoxypyrazines, a class of volatile aromatic compounds, are commonly generated by grape varieties traditionally grown in Bordeaux, such as Cabernet Sauvignon and Sauvignon Blanc. At moderate to low levels, these compounds are considered a desirable and key component of wines fermented from these grapes.

However, at high concentrations, these compounds are considered undesirable because they yield wines that are excessively "vegetal" in their aromatic profile. ARS researchers in Geneva, New York, demonstrated that variation in the concentration of these compounds is quantitatively inherited and controlled by two unlinked genes with large genetic effects. Mapping this trait is the first step in developing an assay that will improve the efficiency for selecting this trait during grape breeding and will lead to further insights into how developing grape berries produce these compounds.

Designing healthy soybean oils for margarines and shortenings. There are two types of saturated fatty acids in soybean oil, palmitic and stearic. Although some saturated fats have been implicated in raising blood serum cholesterol, which is associated with heart disease, stearic acid has been shown to be neutral in this regard. Increasing stearic acid in soybean oil would make hydrogenation, a process used to increase the functionality of soybean oil, but which adds unhealthy trans-fats, less necessary. Global efforts have been underway for the last two decades to raise the saturation of soybean oil by trying to manipulate genes that are highly expressed in the seed. While examining genes that are expressed throughout other plant tissues, ARS scientists in Raleigh, North Carolina, in collaboration with North Carolina State University, identified a novel soybean mutation that, when combined with previously known genes expressed in the seed, significantly raises the saturated fatty acids in soybean oil. Molecular markers were developed to select for these mutated genes. The additive effects for stearic acid obtained when combining these newly discovered genes with previously identified genes increases stearic acid in soybean oil from 4 to 15 percent, a 3.75-fold increase. Breeders are using this new discovery to develop commercial products.

Genetic control of essential dietary minerals in beans. Dry beans (*Phaseolus* species), a staple food world-wide, are a valuable source of dietary zinc (Zn) and iron (Fe) for populations with largely plant-based diets. ARS researchers in East Lansing, Michigan, analyzed dry bean cultivars with different concentrations of zinc and identified genes in two navy bean cultivars with divergent gene expression patterns that yielded a 30 percent difference in seed zinc concentration. They determined that ten differentially expressed genes are involved in Zn or Fe transport in dry beans. The identification of these differentially expressed Zn and Fe transport genes will enable more effective breeding for increased seed Zn and Fe levels in dry beans to benefit human nutrition.